



## SEQUENCE LISTING

<110> Lobb, Roy R.  
Burkly, Linda C.

<120> TREATMENT FOR ASTHMA

<130> 10274-003003

<140> 09/251,073

<141> 1999-02-16

<150> 08/822,830

<151> 1997-03-21

<150> 08/456,193

<151> 1995-05-31

<150> 08/374,331

<151> 1995-01-18

<150> 08/256,631

<151> 1994-07-12

<150> PCT/US93/00030

<151> 1993-01-12

<150> 07/821,768

<151> 1992-01-13

<160> 16

<170> FastSEQ for Windows Version 4.0

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<211> 363

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(363)

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Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

tca gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac acc 96  
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr  
20 25 30

tat atg cac tgg gtg aag cag agg cct gaa cag ggc ctg gag tgg att 144  
Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile  
35 40 45

gga agg att gat cct gcg agt ggc gat act aaa tat gac ccg aag ttc 192  
 Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe  
           50                              55                              60

cag gtc aag gcc act att aca gcg gac acg tcc tcc aac aca gcc tgg 240  
 Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp  
           65                              70                              75                              80

ctg cag ctc agc agc ctg aca tct gag gac act gcc gtc tac tac tgt 288  
 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
                               85                              90                              95

gca gac gga atg tgg gta tca acg gga tat gct ctg gac ttc tgg ggc 336  
 Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly  
                               100                              105                              110

caa ggg acc acg gtc acc gtc tcc tca 363  
 Gln Gly Thr Thr Val Thr Val Ser Ser  
           115                              120

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 Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala  
   1                              5                              10                              15  
 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr  
           20                              25                              30  
 Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile  
           35                              40                              45  
 Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe  
           50                              55                              60  
 Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp  
           65                              70                              75                              80  
 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
                               85                              90                              95  
 Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly  
           100                              105                              110  
 Gln Gly Thr Thr Val Thr Val Ser Ser  
           115                              120

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 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly

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gac agg gtt acc ata acc tgc aag gcc agt cag agt gtg act aat gat				96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp				
20		25	30	
gta gct tgg tac caa cag aag cca ggg cag tct cct aaa ctg ctg ata				144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile				
35		40	45	
tat tat gca tcc aat cgc tac act gga gtc cct gat cgc ttc act ggc				192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly				
50		55	60	
agt gga tat ggg acg gat ttc act ttc acc atc agc act gtg cag gct				240
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala				
65		70	75	80
gaa gac ctg gca gtt tat ttc tgt cag cag gat tat agc tct ccg tac				288
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr				
85		90	95	
acg ttc gga ggg ggg acc aag ctg gag atc				318
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile				
100		105		

<210> 4  
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Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly				
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp				
20		25	30	
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile				
35		40	45	
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly				
50		55	60	
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala				
65		70	75	80
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr				
85		90	95	
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile				
100		105		

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 <222> (1)...(1338)

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Met	Pro	Gly	Lys	Met	Val	Val	Ile	Leu	Gly	Ala	Ser	Asn	Ile	Leu	Trp	
1				5					10						15	

ata	atg	ttt	gca	gct	tct	caa	gct	ttt	aaa	atc	gag	acc	acc	cca	gaa	96
Ile	Met	Phe	Ala	Ala	Ser	Gln	Ala	Phe	Lys	Ile	Glu	Thr	Thr	Pro	Glu	
			20					25					30			

tct	aga	tat	ctt	gct	cag	att	ggg	gac	tcc	gtc	tca	ttg	act	tgc	agc	144
Ser	Arg	Tyr	Leu	Ala	Gln	Ile	Gly	Asp	Ser	Val	Ser	Leu	Thr	Cys	Ser	
		35					40					45				

acc	aca	ggc	tgt	gag	tcc	cca	ttt	ttc	tct	tgg	aga	acc	cag	ata	gat	192
Thr	Thr	Gly	Cys	Glu	Ser	Pro	Phe	Phe	Ser	Trp	Arg	Thr	Gln	Ile	Asp	
	50					55					60					

agt	cca	ctg	aat	ggg	aag	gtg	acg	aat	gag	ggg	acc	aca	tct	acg	ctg	240
Ser	Pro	Leu	Asn	Gly	Lys	Val	Thr	Asn	Glu	Gly	Thr	Thr	Ser	Thr	Leu	
	65				70					75					80	

aca	atg	aat	cct	gtt	agt	ttt	ggg	aac	gaa	cac	tct	tac	ctg	tgc	aca	288
Thr	Met	Asn	Pro	Val	Ser	Phe	Gly	Asn	Glu	His	Ser	Tyr	Leu	Cys	Thr	
				85					90					95		

gca	act	tgt	gaa	tct	agg	aaa	ttg	gaa	aaa	gga	atc	cag	gtg	gag	atc	336
Ala	Thr	Cys	Glu	Ser	Arg	Lys	Leu	Glu	Lys	Gly	Ile	Gln	Val	Glu	Ile	
			100					105					110			

tac	tct	ttt	cct	aag	gat	cca	gag	att	cat	ttg	agt	ggc	cct	ctg	gag	384
Tyr	Ser	Phe	Pro	Lys	Asp	Pro	Glu	Ile	His	Leu	Ser	Gly	Pro	Leu	Glu	
		115					120					125				

gct	ggg	aag	ccg	atc	aca	gtc	aag	tgt	tca	gtt	gct	gat	gta	tac	cca	432
Ala	Gly	Lys	Pro	Ile	Thr	Val	Lys	Cys	Ser	Val	Ala	Asp	Val	Tyr	Pro	
	130					135					140					

ttt	gac	agg	ctg	gag	ata	gac	tta	ctg	aaa	gga	gat	cat	ctc	atg	aag	480
Phe	Asp	Arg	Leu	Glu	Ile	Asp	Leu	Leu	Lys	Gly	Asp	His	Leu	Met	Lys	
145					150					155					160	

agt	cag	gaa	ttt	ctg	gag	gat	gca	gac	agg	aag	tcc	ctg	gaa	acc	aag	528
Ser	Gln	Glu	Phe	Leu	Glu	Asp	Ala	Asp	Arg	Lys	Ser	Leu	Glu	Thr	Lys	
				165					170					175		

agt	ttg	gaa	gta	acc	ttt	act	cct	gtc	att	gag	gat	att	gga	aaa	gtt	576
Ser	Leu	Glu	Val	Thr	Phe	Thr	Pro	Val	Ile	Glu	Asp	Ile	Gly	Lys	Val	
			180					185					190			

ctt	gtt	tgc	cga	gct	aaa	tta	cac	att	gat	gaa	atg	gat	tct	gtg	ccc	624
Leu	Val	Cys	Arg	Ala	Lys	Leu	His	Ile	Asp	Glu	Met	Asp	Ser	Val	Pro	
		195					200					205				

aca	gta	agg	cag	gct	gta	aaa	gaa	ttg	caa	gtc	gac	aaa	act	cac	aca	672
Thr	Val	Arg	Gln	Ala	Val	Lys	Glu	Leu	Gln	Val	Asp	Lys	Thr	His	Thr	
	210					215					220					

tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe 225 230 235 240	720
ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro 245 250 255	768
gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val 260 265 270	816
aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr 275 280 285	864
aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc gtc Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val 290 295 300	912
ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys 305 310 315 320	960
aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser 325 330 335	1008
aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro 340 345 350	1056
tee cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val 355 360 365	1104
aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly 370 375 380	1152
cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp 385 390 395 400	1200
ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp 405 410 415	1248
cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His 420 425 430	1296
aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 435 440 445	1338
tgagtgcgg	1347

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 <223> Primer

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24

<210> 7  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Primer

<400> 7  
 gtaaattgagt gcggcgggccg ccaa

24

<210> 8  
 <211> 115  
 <212> DNA  
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<220>  
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<400> 8  
 gcggcgcggg- tccaaccacc aatctcaaag-cttggtaccc ggggaattcag atctgcagca  
 tgctcgagct ctagatatcg attccatgga tctcacatc ccaatccgcg gccgc

60

115

<210> 9  
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<400> 9  
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41

<210> 10  
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 <212> DNA  
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 <223> Primer

<400> 10  
 aagtcgactt gcaattcttt tac

23

<210> 11  
 <211> 14  
 <212> DNA  
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<220>  
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<400> 11  
 tcgacgcggc cgcg

14

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tca gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac acc 96  
 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr  
 20 25 30

tat atg cac tgg gtg aag cag agg cct gaa cag ggc ctg gag tgg att 144  
 Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile  
 35 40 45

gga agg att gat cct gcg agt ggc gat act aaa tat gac ccg aag ttc 192  
 Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe  
 50 55 60

cag gtc aag gcc act att aca gcg gac acg tcc tcc aac aca gcc tgg 240  
 Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp  
 65 70 75 80

ctg cag ctc agc agc ctg aca tct gag gac act gcc gtc tac tac tgt 288  
 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

gca gac gga atg tgg gta tca acg gga tat gct ctg gac ttc tgg ggc 336  
 Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly  
 100 105 110

caa ggg acc acg gtc acc gtc tcc tca 363  
 Gln Gly Thr Thr Val Thr Val Ser Ser  
 115 120

<210> 13  
 <211> 121  
 <212> PRT

<213> Homo sapiens

<400> 13

Gln	Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala
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Ser	Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr
	20						25					30			
Tyr	Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile
	35					40					45				
Gly	Arg	Ile	Asp	Pro	Ala	Ser	Gly	Asp	Thr	Lys	Tyr	Asp	Pro	Lys	Phe
50					55					60					
Gln	Val	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Trp
65				70				75						80	
Leu	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
		85						90					95		
Ala	Asp	Gly	Met	Trp	Val	Ser	Thr	Gly	Tyr	Ala	Leu	Asp	Phe	Trp	Gly
	100							105				110			
Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser							
	115						120								

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<212> PRT

<213> Artificial Sequence

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<223> Synthetically generated peptide

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<210> 15

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated peptide

<400> 15

Met	Pro	Gly	Lys	Met	Val	Val
1			5			

<210> 16

<211> 5

<212> PRT

<213> Homo sapiens

<400> 16

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1			5	